

METHODS OF IDENTIFYING POINT MUTATIONS IN A GENOME

ABSTRACT OF THE DISCLOSURE

The invention relates to a method for identifying inherited point mutations in a targeted region of the genome in a large population of individuals and determining
5 which inherited point mutations are deleterious, harmful or beneficial. Deleterious mutation are identified directly by a method of recognition using the set of point mutations observed in a large population of juveniles. Harmful mutations are identified by comparison of the set of point mutation observed in a large set of juveniles and a large set of aged individuals of the same population. Beneficial mutations are similarly
10 identified.

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